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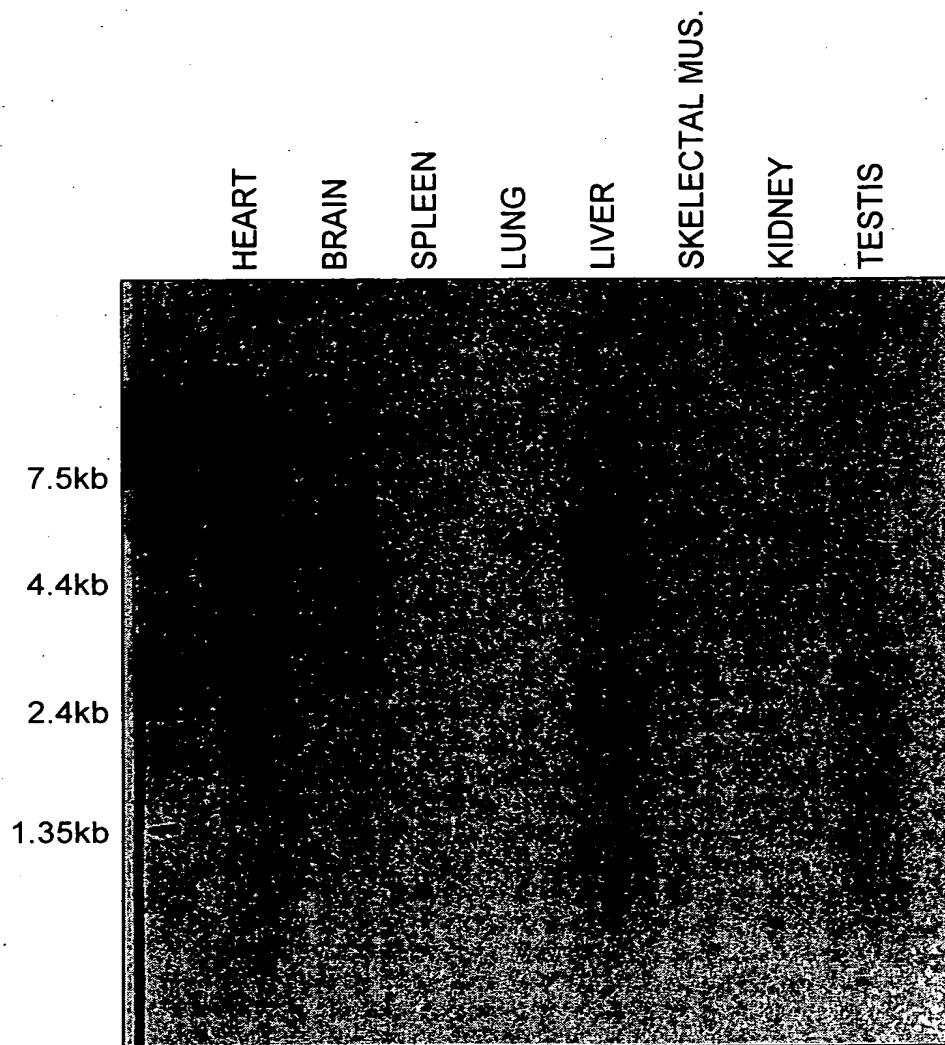


FIG. 1
MURINE MTN BLOT PROBED WITH
³²P-LABELLED MURINE PDE_XIV

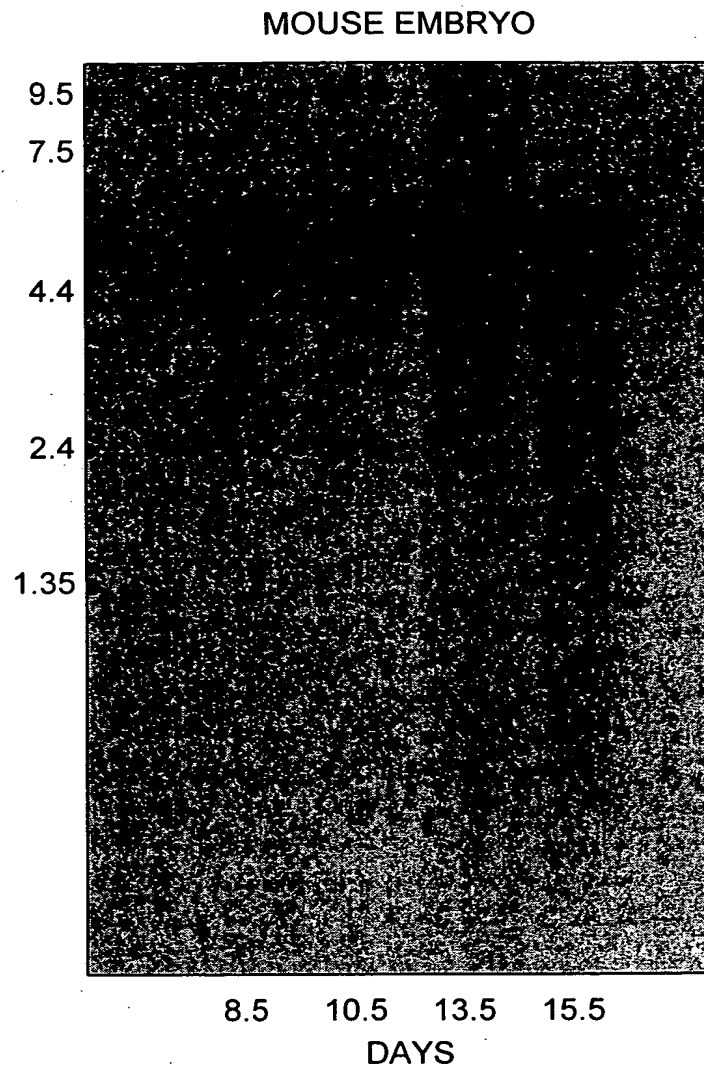
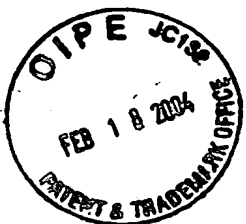


FIG. 2

MURINE EMBRYO MTN BLOT PROBED
WITH ^{32}P -LABELLED MURINE PDE_{XIV}



	1	2	3	4	5	6	7	8
A	WHOLE BRAIN	AMYG- DALA	CAUDATE NUCLEUS	CERE- BELLUM	CEREBAL CORTEX	FRONTAL LOBE	HIPPO- CAMPUS	MEDULLA OBLON- GATA
B	OCCIP- ITAL LOBE	PUTAMEN	SUBST- ANTIAL NIGRA	TEMP- ORAL LOBE	THALA- MUS	NUCLEUS ACCUM- BEUS	SPINAL CORD	
C	HEART	SORTA	SKELETAL MUSCLE	COLON	BLADDER	UTERUS	PROST- ATE	STOMACH
D	TESTIS	OVARY	PANC- REAS	PITUIT- ARY GLAND	ADRENAL GLAND	THYROID GLAND	SALIVARY GLAND	MAMM- ARY GLAND
E	KIDNEY	LIVER	SMALL INTE- STINE	SPLEEN	THYMUS	PERIPH- ERAL LEUKO- CYTE	LYMPH NODE	BONE MARROW
F	APPEN- DIX	LUNG	TRACHEA	PLACEN- TA				
G	FETAL BRAIN	FETAL HEART	FETAL KIDNEY	FETAL LIVER	FETAL SPLEEN	FETAL THYMUS	FETAL LUNG	
H	YEAST TOTAL RNA 100ng	YEAST IRNA 100ng	E. COLI RNA 100ng	E. COLI DNA 100ng	POLY r(A) 100ng	HUMAN C ₀ 11 DNA 100ng	HUMAN DNA 100ng	HUMAN DNA 500ng

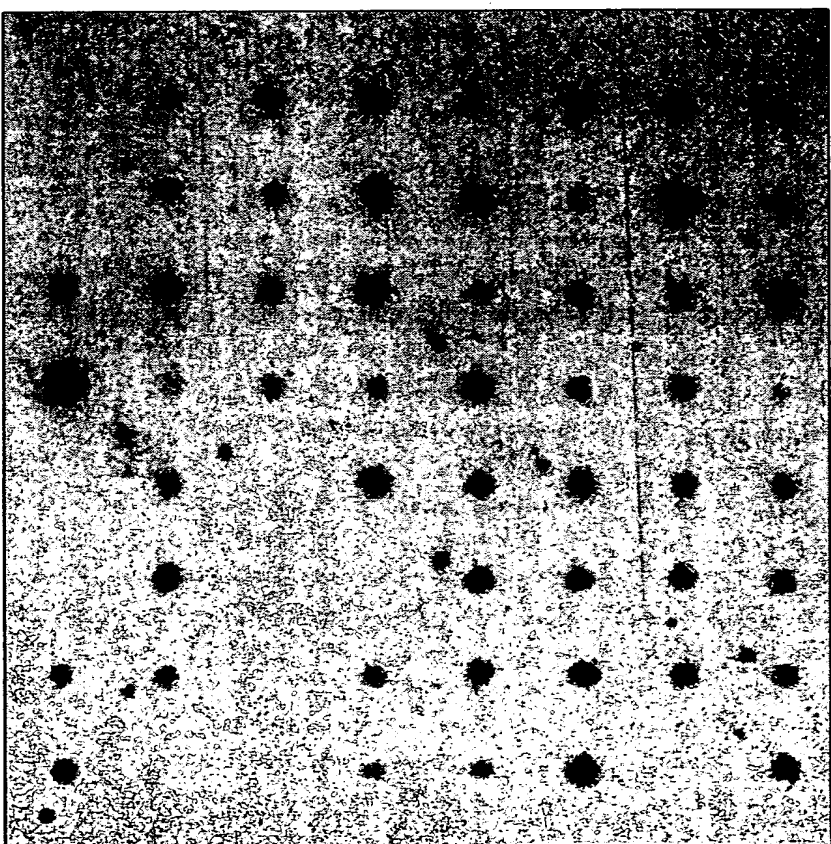


FIG. 3

HUMAN RNA MASTER BLOT PROBED WITH
32P-LABELLED HUMAN PDE_XIV



FIG. 4

Alignment of the Murine and Human PDE_XIV nucleotide sequence

New sequence is PDE_XIV

Fileup: Genetics Computer Group.

MSF: 3134 Type: N Check: 5422 ..

Name: mpdea_oo Len: 3134 Check: 5084 Weight: 0.001

Name: hspdea_oo Len: 3134 Check: 338 Weight: 0.100

```
new mpde_      1 AGGTACGCCT GCAGGTACCG GTCCGGAATT CCCGGGTCGA CCCACGCGTC
new hspde_      .....

new mpde_      51 CGGCCAGCCT CCCAGGCCGG CTGCCTGCTC ACCCAGCCAG TCGCTAGCTC
new hspde_      1 ..... .CGGAAT.TC

mpdea_         101 TGGGCAC TGC AGCAGGCTCG GCTCTGTCCC AGCGCTCGCT TGCTTGCTCG
hspde_          9 GATGCAC TGC AGCAGGCTCG GCTCTGTCCC AGC....A..

mpdea_         151 CTCGCTCGGC TGGGAGAAAA GTGGTGTC.C TCGCCCAG.. AGAGCCTCTC
hspde_          43 ....CTTGTC TGGGAGAAAA GTGGTGTTAC TCACCCAGGG AGAGTCTCTC

mpdea_         198 TCTC..CCTT CCTTCTTTCT CGAGCTCTCT GAGTCCTTTG GCGTTTCTTT
hspde_          89 TTTCTACCTT CCTTCTTTCT CGATCTCCTT GTGTGCTTTT GTGTTTCTTT

mpdea_         246 CTTTCTTTTC TTTTTTTTTT TTTTAAATA TTTTCTTTT CTTTCTATAA
hspde_        139 ATTTCTTTTC CTTTTTTTTC TT..... TTTTTTTTTT GTTACT....

mpde_          296 AACTTG CATA ATTATACTGC TAATCCTGGA TGAGGTTGCT GGATTCTGCA
hspde_        177 .....TA ATTATATTCC TAATCCTGGA TGAAGTTGCT GGATTCTGCA

mpde_          346 GCACAAATCT TCATGAACAA GCCGCACCGC TCAGAGATTT CACAGCATTC
hspde_        219 GCACAAGTCT TCATGAACAA GCAGCACCGC TCAGAGATTT CACGGCATTC

                                start codon
mpde_          396 AAAGGTCACA GAACTGCCAC TATGGTTAAA TGTCTTGTTT AATGGTTGAG
hspde_        269 AAAGGTCACA GAACTGCCAC TATGGTTAAA TGTCTTGTTT AATGGTTGAG

mpdea_         446 AGGTGTGGCG AAGTCTTGTT TGAGAGCCCT GAACAGAGTG TCAAATGTGT
hspde_        319 AGGTGTGGCG AAATCTTGTT TGAGAACCCC GATCAGAATG CCAAATGTGT

mpde_          496 TTGCATGCTA GGAGATGTAC GACTAAGGGG TCAGACGGGG GTTCCTGCCG
hspde_        369 TTGCATGCTG GGAGATATAC GACTAAGGGG TCAGACGGGG GTTCGTGCTG

mpde_          546 AACGCCGTGG CTCCTACCCA TTCATTGACT TCCGTCTACT TAACAATACA
hspde_        419 AACGCCGTGG CTCCTACCCA TTCATTGACT TCCGCTACT TAACAGTACA

mpde_          596 ACACACTCAG GGGAAATTGG CACCAAGAAA AAGGTGAAAC GACTGTTAAG
hspde_        469 ACATACTCAG GGGAGATTGG CACCAAGAAA AAGGTGAAA GACTATTAAG

mpde_          646 TTTCAAAGA TACTTCCATG CATCTAGGCT TCTCCGGGGG ATTATACCGC
hspde_        519 CTTTCAAAGA TACTTCCATG CATCAAGGCT GCTTCGTGGA ATTATACCAC

mpde_          696 AGGCCCCCTCT CCACCTGCTG GATGAAGACT ACCTTGACA AGCAAGGCAC
hspde_        569 AAGCCCCCTCT GCACCTGCTG GATGAAGACT ACCTTGACA AGCAAGGCAT

mpde_          746 ATGCTCTCCA AAGTTGGAAC GTGGGACTTT GACATTTTCT TGTTTGATCG
hspde_        619 ATGCTCTCCA AAGTGGAAT GTGGGATTTT GACATTTTCT TGTTTGATCG
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FIG. 4 CONTD

mpde_	796	CTTGACAAAT	GGGAACAGTC	TGGTAACTCT	GTTGTGTCAC	CTCTTCAACT
hspde_	669	CTTGACAAAT	GGAAACAGCC	TGGTAACACT	GTTGTGCCAC	CTCTTCAATA
mpde_	846	CCCATGGGCT	CATCCACCAT	TTCAAGCTCG	ATATGGTGAC	CTTGCACAGG
hspde_	719	CCCATGGACT	CATTCACCAT	TTCAAGTTAG	ATATGGTGAC	CTTACACCGA
mpde_	896	TTTCTGGTTA	TGGTTCAGGA	AGATTACCAC	GGTCACAACC	CATACCACAA
hspde_	769	TTTTTAGTCA	TGGTTCAGA	AGATTACCAC	AGCCAAAACC	CGTATCACAA
mpde_	946	TGCTGTTCAC	GCAGCCGACG	TCACCCAGGC	CATGCACTGT	TACCTGAAGG
hspde_	819	TGCTGTTCAC	GCAGCCGACG	TCACCCAGGC	CATGCACTGC	TACCTGAAAG
mpde_	996	AGCCAAAAGTT	GGCAAGCTTC	CTCACACCTC	TGGACATCAT	GCTTGGACTA
hspde_	869	AGCCAAAAGCT	TGCCAGCTTC	CTCACGCCTC	TGGACATCAT	GCTTGGACTG
mpde_	1046	CTGGCTGCAG	CAGCTCATGA	CGTGGACCAC	CCAGGGGTCA	ACCAGCCATT
hspde_	919	CTGGCTGCAG	CAGCACACGA	TGTGGACCAC	CCAGGGGTGA	ACCAGCCATT
mpde_	1096	TTTGATCAAA	ACTAACCACC	ATCTTGCCAA	CCTGTATCAG	AATATGTCTG
hspde_	969	TTTGATAAAA	ACTAACCACC	ATCTTGCCAA	CCTATATCAG	AATATGTCTG
mpde_	1146	TACTGGAGAA	TCACCACTGG	CGATCTACAA	TTGGCATGCT	TCGAGAATCA
hspde_	1019	TGCTGGAGAA	TCATCACTGG	CGATCTACAA	TTGGCATGCT	TCGAGAATCA
mpde_	1196	CGGCTCCTGG	CTCACTTGCC	AAAGGAAATG	ACACAGG...ATATC
hspde_	1069	AGGCTTCTTG	CTCATTTGCC	AAAGGAAATG	ACGTAAGTGC	TGCCGAGATG
					stop codon	
mpde_	1238	GAACA.....GCA...GCTG	GGCTCCCTCA	TCTTGGCCAC
hspde_	1119	AAACATACTG	ATGTGCATGC	AGTAAAGATA	AGCCACTTTC	TCTAGGGCA.
mpde_	1270	GGATATCAAC	AGACAGAATG	AGTTTCTGA.CCCG	CTTAAAGCT
hspde_	1168	GGCTTGGGAC	CTTTTGCGTG	AATGGCAGAG	AGCCCCCGG	CTGTACTTCC
mpde_	1313	CACCTCCACA	ATAAAGATT.	TGAGAC....	..TGGAGAAT	GT.ACAGGA.
hspde_	1218	TGCCTGCACT	GAGCTGTCTA	TCAGAGGAGA	TTTGGTGTCA	GTTACAGCAA
mpde_	1354	..CAGACACT	TTATGCT.TC	AGATCGCCTT	GAAGTGTGCT	GACATTTGCA
hspde_	1268	CCCAGAAACC	AAAATCTCTC	TGTGTGCTTT	GAAAGGGCCT	TGCAGAGTCA
mpde_	1401	AT..CCTT..	GTC.GTATCT	GGGAGATGAG	CAAGCAGT..	GGAGTGAAG
hspde_	1318	ATGACCTACA	GTCAGGAAAA	GGGATAATAA	ACAGCTCTCA	GTTTCACAC
mpde_	1444	GGT.....	CTGTGAGGAA	TTCTACAGAC	AAGGTGACCT	TGAAC..AG.
hspde_	1368	GCTTCAGTAT	CAGTGCTCAA	CTTTGCCAA	TTCCCGACCT	TTAGTTTAGC
mpde_	1484	AAGTTTGAAC	TGGAAATCAG	.TCCTCTTTG	TAATCAAC.A	GAAAGATTCA
hspde_	1418	AAAATTGTCC	TTCCATGTAG	CTCCAAATAG	TAAATATTTA	TCAAGAAGGA
mpde_	1532	ATCCCTAGCA	TACAAA...T	TGGTTTCATG	ACT.TACATC	GTGGAGCCGC
hspde_	1468	A.CCCAGGCA	TTCTAAAGCT	AGAGTTCAAA	AAAGTATATT	TTGTAATTGC
mpde_	1578	TGTTCCGGG.	...AGTGG..	GCCCCGTTTA	CTGGG..AAC	AGCACCCCTGT
hspde_	1517	TAGTCTCAGC	AAAAATAGAA	GTCAGAAATT	CTTTTCTAAA	ATGTCTTTTG
mpde_	1620	CGGAGAACAT	GCTAAGCC..ATCTCG	CGCACAACAA	AGCCAGTGG
hspde_	1567	CTAAGTAATT	GAAATGGCCC	TAGCATTTTT	TTACCAATT	AATTTACCTT
mpde_	1664	AAGAGCCT.G	CTGTCCAATC	AGCAC...AG	ACGCA.....	...GGGGCAG
hspde_	1617	ACGTCTCTTG	CACTTTAAAC	AGAAGGGGAG	ACACTCATT	TCTGGTTTCA
mpde_	1702	CG.....G	CCAGGACCTG	GCGG...GC	CCCGC...AC	CTGAGACCCT
hspde_	1667	TATTTGATAG	CCATGGTATG	TAGGCTGAGT	CCCACTAAAT	CTGAGGCCAT

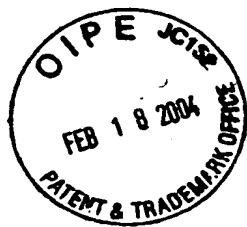


FIG. 4CONT'D

				stop codon		
mpde_	1738	GGAG.CAGAC	AGAAGGTGCC	ACGCCCTAAG	GTAGCTGTC.	.TGCTGA..T
hspde_	1717	TGTTTCATTT	TCCTGGTG..	..GCCCAAG	TTAGCTGCTA	ATACTGTCTT
mpde_	1783	GCACGGCCA.TCT	G.TCCGTCCACAGGA	GCACGGCC..
hspde_	1763	CCAAGGCCAC	CATTAATTCT	GATCTGTTTA	ATGAACACGT	GCAGAACCCA
mpde_	1817	...ATCC...G	TCC...GACT	GC.....	.CCTCGCAAC
hspde_	1813	AGAAACCTAG	GTGAAAAGAG	TACATAGATT	GCTGTACCCT	TCTTCAAGAC
mpde_	1840	AAGCCCATCA	CGCTGGGTTT	CGATGCCAT.	.CCGCCTGCC	A.CTTACC..
hspde_	1863	AAGCACATAA	CTTGAGGTCA	AGGACCAAGT	GCTGTCTCCC	AACTGAACAA
mpde_	1885	...GCCTCCC	TTCGTTGATC	CAAGTGATCA	AAAGCCATTG	...TCACCTC
hspde_	1913	GCAGTATACT	CTGGGTTGTG	GATTGATTCC	TGGCCCTCTG	ATTTGATCTC
mpde_	1929	AGCAT.....	.TAGCTGCC.	..GAAATGGG	CGGCTCTATC	CCGTCATTGG
hspde_	1963	ATGCTGTTTC	CTAGCACCCA	GAGGAATGTG	AAATTTGCAG	GAGGAATTTT
mpde_	1970	AG..CTGAT.	...TCTGGGG	CGGCTGCCCC	AACCGAAAC.G
hspde_	2013	AGTTCTGATA	AATTTTFACT	CCCTGGAAC	AAATAAAACC	AGTTCTCGTG
mpde_	2004	CCTGGAAGTA	AGAA..AGGG	GTGCTTCTGC	CGTGTTCCGC	TCTGGCCCTT
hspde_	2063	CATGGAATAA	AAACTTATGC	CTCTTACTAG	AATAATAAAT	TGCAAAGATT
mpde_	2052	GGTCACGCTG	ACTGGCAGTA	GCTCCTAAGT	CCAGAGCATT	TTAACGTTTG
hspde_	2113	GAAAGAATTA	AATGCAAAAA	GAATAAAAA	CTAGAGCAAA	AGATCAAGTG
mpde_	2102	CCATC..GGA	CAGCTGACCT	...GCATGAC	ACCAGCAT..	.ACTTGGAAC
hspde_	2163	AGAAGAAGAA	AAGAGGAGGT	AAGGAGAGAG	ACAAGGAAGA	AAGAAGGAGA
mpde_	2144	TGCAAAACTG	GTCTTGCGTG	CCAGAGCACA	AACGAGAGTG	TGAGAGAAA.
hspde_	2213	AGGAAAGGAA	GAATAGTGAG	G.ACAGGAAA	GAAGAAAATG	CAAGGGAAAT
mpde_	2193	..GTACCTTC	TATTT..TAA	TAATAATTAT	TATTATAAAA	TA....ATAA
hspde_	2262	GGGAAAGGAC	TCTGGGGTGA	CCAGACTTCT	CCTGGTCAGT	ACCTGCATTC
mpde_	2235	ATCTTTTTTAA	CTTTT..ATA	TTTCATGCAC	CAGACAATGG	GTCTAAAACT
hspde_	2312	ATCCTGTTTG	TTACTCAATA	TTTCTTTCCT	AAAATATTCA	TTTCACATCT
mpde_	2283	TTGGA...CA	AGTAATACTC	TGCGTACCCA	AACCTAAGAG	G.....GGG
hspde_	2362	ATGGATTCCA	ATGAAAAATA	TATTTTATG	TGTCTTTGTG	GAACACAGTG
mpde_	2324	TTC...ATTA	TTTT.GCTAT	T.GACTC...	..TATGCCAC	ATTGGGTCCG
hspde_	2412	TTATAAATTG	TTTTTGCCAG	AAGAATAATT	GTTATACAAT	AATATATGTG
mpde_	2364	AGA..TGTGG	CACCATTGCG	ATTTCTGAAA	CCACGCGTCC	.CCTCCCATC
hspde_	2462	AAAACTTTAT	TACAAAAGCC	ATTATCATAA	TCATTATTAT	TCCTTCTATC
mpde_	2411	TGGTGGAAGG	TGCTGTACAG	CCCGTCCC..	..TTTGCACC	GTTAGCCAAT
hspde_	2512	ACA.GGTAAA	TGCTTTAATG	TCATTTTTCT	GATTTTAAAA	GTAGGGCAGG
mpde_	2457	CCGTCTTT..TACGGA	...TTCAGTG	ACCTGTTTAT	ATTACAA..G
hspde_	2561	TTAATTGTAG	AAAGTAAGGA	AAATTCAGGA	AAGTGTTAGT	TTGAACATG
mpde_	2497	TGTACATTTT	CTGT..AAAT	ACCAAACGCT	ACTGA.....TTCC
hspde_	2611	TGAAGTTGCT	CTTTTAAAGG	GCCAAAAACA	GGAGACTTTT	AGCACTTTCA
mpde_	2534	CATGC..CA.AAATAC	ACGAGTATTA	TGGGATTGCT	A.....CCTG
hspde_	2661	TATGTTTCAG	CTTGATATGA	AAGAGAAAAC	TGAAACTGCT	AGTAATCCTG
mpde_	2571T	ATAAACAATG	GCACTGTGAA	CAGAATA...	.CTGTTAGTT
hspde_	2711	CCATCCAGGT	ATAGTTCATG	TTAACCTGGC	TAGTTTATTT	TCTTTTAGTC



FIG. 4_{CONT'D}

mpde_	2608	TTAATACAAG	AGAATGCATT	TGTAAATATG	GTATAGAGTT	TATTAATATA
hspde_	2761	TTTTTTTCAAT	ACAAA.CTTA	TTTAAACAAA	ATAT.GATTA	TATTTGGGGA
mpde_	2658	CTGTTGTTCG	CAGATAAAGG	CCTTAACTTT	AAAAAAAAAA	AAAAAAAAA.
hspde_	2809	ACTTATTTTA	CAGTTTACGT	CCTGAAATTT	TTTATTTACA	ATAAAGACTT
mpde_	2708AAAA	AAAAAAAAAA	AAAAAGGGGC	GGCCGCTCTA	GAGGATCCCT
hspde_	2859	TTTTCCAAAT	CAAAAAAAAA	AAAAAAGGGC	GGCCGCTCTA	GAGGATCCCT
mpde_	2752	CGAGGGGCCC	AAGCTTACGC	GTGCATGCGA	CGTCATAGCT	CTCTCCCTAT
hspde_	2909	CGAGGGGCCC	AAGCTTACGC	GTGCATGCGA	CGTCATAGCT	CTCTCCCTAT
mpde_	2802	AGTGAGTCGT	ATTATAAGCT	AG.....	2823
hspde_	2959	AGTGAGTCGT	ATTATAAGCT	AGGCACTGGC	CGTC	2992



FIG. 5

Protien Alignment of the Murine & Human PDE_{XIV}

CLUSTAL W (1.7) multiple sequence alignment

```
mpde      MSCLMVERCGEVLFESPEQSVKVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60
hspde     MSCLMVERCGEILFENPDQNACVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
          *****:***:*.*****:*****
mpde      GEIGTKKKVKRLLSFQRYFHASRLLGIIPQAPLHLLDELYLGQARHMLSKVGTWDFDIF 120
hspde     GEIGTKKKVKRLLSFQRYFHASRLLGIIPQAPLHLLDELYLGQARHMLSKVGMWDFDIF 120
          *****
mpde      LFDRLTNGNSLVTLLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHPYHNAVHAAD 180
hspde     LFDRLTNGNSLVTLLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
          *****
mpde      VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLKTNHHLANLYQNMS 240
hspde     VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLKTNHHLANLYQNMS 240
          *****
mpde      VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
hspde     VLENHHWRSTIGMLRESRLLAHLPKEMT----- 268
          *****
mpde      KDLRLENVQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360
hspde     -----
mpde      PLCNQKQDSIPSIIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420
hspde     -----
mpde      HRRRGSGQDLAGPAPETLEQTEGATP 446
hspde     -----
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Zinc binding motif's are highlighted in bold.
Non-Catalytic domain in italics.

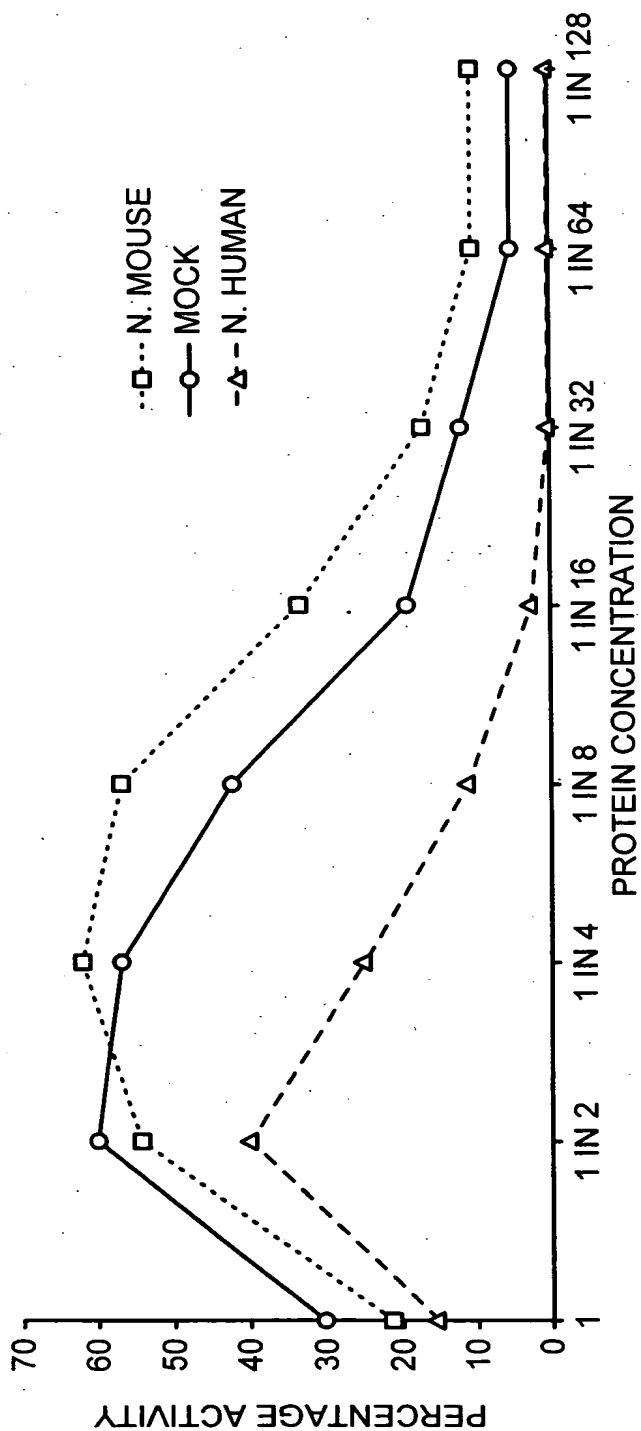


FIG. 6

SPA ASSAY TO DETERMINE THE cAMP HYDROLYTIC
ACTIVITY OF MURINE AND HUMAN PDE_XIV